

1643

Serial Number: 09/501/171A

ENTERED

#4

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☒ Other: Seq 4, 6 - corrected amino acid numbering

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JUN 26 2001

TECH CENTER 1600/2900

RAW SEQUENCE LISTING

DATE: 06/08/2000

PATENT APPLICATION: US/09/501,171A

TIME: 10:48:01

Input Set : A:\Pto.amc

Output Set: N:\CRF3\06082000\I501171A.raw

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4 <110> APPLICANT: St. George-Hyslop, Peter H.
5   Fraser, Paul E.
7 <120> TITLE OF INVENTION: Proteins Related to Neuronal
8   Regeneration and Uses Thereof
10 <130> FILE REFERENCE: 1034/1F811
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/501,171A
C--> 12 <141> CURRENT FILING DATE: 2000-02-09
12 <160> NUMBER OF SEQ ID NOS: 6
14 <170> SOFTWARE: FastSEQ for Windows Version 3.0
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17 <211> LENGTH: 467
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19 <213> ORGANISM: human
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25   20                               25          30
26 Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His Pro Glu
27   35                               40          45
28 Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val Val Glu
29   50                               55          60
30 Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys
31   65                               70          75          80
32 His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val
33   85                               90          95
34 Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln
35   100                              105          110
36 Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg
37   115                              120          125
38 Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Ile Val
39   130                              135          140
40 Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys
41   145                              150          155          160
42 Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Phe Phe
43   165                              170          175
44 Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn Val Ala
45   180                              185          190
46 Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Phe Gly Val Val
47   195                              200          205
48 Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala
49   210                              215          220
50 Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr
51   225                              230          235          240
52 Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr
53   245                              250          255
54 Asp Leu Val Ala Val Leu Cys Pro Lys Gly Pro Leu Arg Met Leu Val

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56 Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr
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58 Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu
59      290      295      300
60 Ala Gln Arg Arg Val Ser Lys Asn Ser Lys Tyr Asn Ala Glu Ser Thr
61      305      310      315      320
62 Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly Gly Phe
63      325      330      335
64 Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg
65      340      345      350
66 Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser Ser Ile
67      355      360      365
68 Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly
69      370      375      380
70 Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala
71      385      390      395      400
72 Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile
73      405      410      415
74 Gly Leu Cys Leu Thr Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu
75      420      425      430
76 Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala
77      435      440      445
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80 Phe Tyr Ile
81 465
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94 35 40 45
95 Ser Gln Glu Asn Glu Glu Asp Gly Glu Glu Asp Pro Asp Arg Tyr Val
96 50 55 60
97 Cys Ser Gly Val Pro Gly Arg Pro Pro Gly Leu Glu Glu Leu Thr
98 65 70 75 80
99 Leu Lys Tyr Gly Ala Lys His Val Ile Met Leu Phe Val Pro Val Thr
100 85 90 95
101 Leu Cys Met Ile Val Val Val Ala Thr Ile Lys Ser Val Arg Phe Tyr
102 100 105 110
103 Thr Glu Lys Asn Gly Gln Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr
104 115 120 125
105 Pro Ser Val Gly Gln Arg Leu Leu Asn Ser Val Leu Asn Thr Leu Ile

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|-----|--|-----|-----|-----|
| 106 | 130 | 135 | 140 | |
| 107 | Met Ile Ser Val Ile Val Val Met Thr Ile Phe Leu Val Val Leu Tyr | | | |
| 108 | 145 | 150 | 155 | 160 |
| 109 | Lys Tyr Arg Cys Tyr Lys Phe Ile His Gly Trp Leu Ile Met Ser Ser | | | |
| 110 | 165 | 170 | 175 | |
| 111 | Leu Met Leu Leu Phe Leu Phe Thr Tyr Ile Tyr Leu Gly Glu Val Leu | | | |
| 112 | 180 | 185 | 190 | |
| 113 | Lys Thr Tyr Asn Val Ala Met Asp Tyr Pro Thr Leu Leu Leu Thr Val | | | |
| 114 | 195 | 200 | 205 | |
| 115 | Trp Asn Phe Gly Ala Val Gly Met Val Cys Ile His Trp Lys Gly Pro | | | |
| 116 | 210 | 215 | 220 | |
| 117 | Leu Val Leu Gln Gln Ala Tyr Leu Ile Met Ile Ser Ala Leu Met Ala | | | |
| 118 | 225 | 230 | 235 | 240 |
| 119 | Leu Val Phe Ile Lys Tyr Leu Pro Glu Trp Ser Ala Trp Val Ile Leu | | | |
| 120 | 245 | 250 | 255 | |
| 121 | Gly Ala Ile Ser Val Tyr Asp Leu Val Ala Val Leu Cys Pro Lys Gly | | | |
| 122 | 260 | 265 | 270 | |
| 123 | Pro Leu Arg Met Leu Val Glu Thr Ala Gln Glu Arg Asn Glu Pro Ile | | | |
| 124 | 275 | 280 | 285 | |
| 125 | Phe Pro Ala Leu Ile Tyr Ser Ser Ala Met Val Trp Thr Val Gly Met | | | |
| 126 | 290 | 295 | 300 | |
| 127 | Ala Lys Leu Asp Pro Ser Ser Gln Gly Ala Leu Gln Leu Pro Tyr Asp | | | |
| 128 | 305 | 310 | 315 | 320 |
| 129 | Pro Glu Met Glu Glu Asp Ser Tyr Asp Ser Phe Gly Glu Pro Ser Tyr | | | |
| 130 | 325 | 330 | 335 | |
| 131 | Pro Glu Val Phe Glu Pro Pro Leu Thr Gly Tyr Pro Gly Glu Leu | | | |
| 132 | 340 | 345 | 350 | |
| 133 | Glu Glu Glu Glu Glu Arg Gly Val Lys Leu Gly Leu Gly Asp Phe Ile | | | |
| 134 | 355 | 360 | 365 | |
| 135 | Phe Tyr Ser Val Leu Val Gly Lys Ala Ala Ala Thr Gly Ser Gly Asp | | | |
| 136 | 370 | 375 | 380 | |
| 137 | Trp Asn Thr Thr Leu Ala Cys Phe Val Ala Ile Leu Ile Gly Leu Cys | | | |
| 138 | 385 | 390 | 395 | 400 |
| 139 | Leu Thr Leu Leu Leu Leu Ala Val Phe Lys Lys Ala Leu Pro Ala Leu | | | |
| 140 | 405 | 410 | 415 | |
| 141 | Pro Ile Ser Ile Thr Phe Gly Leu Ile Phe Tyr Phe Ser Thr Asp Asn | | | |
| 142 | 420 | 425 | 430 | |
| 143 | Leu Val Arg Pro Phe Met Asp Thr Leu Ala Ser His Gln Leu Tyr Ile | | | |
| 144 | 435 | 440 | 445 | |
| 146 | <210> SEQ ID NO: 3 | | | |
| 147 | <211> LENGTH: 4746 | | | |
| 148 | <212> TYPE: DNA | | | |
| 149 | <213> ORGANISM: human | | | |
| 151 | <400> SEQUENCE: 3 | | | |
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| 153 | gcaaggtcag gacottgcct tgaaagccgg gcggcgccgc gcaacgcctc ttcccggact | 120 | | |
| 154 | gaggagctgt cgccggcgga ggggtcatgt ttgcgaggaa gccgcggggc gccgcgcctt | 180 | | |
| 155 | tgggagctat gcctgttcca gaccagcctt catcagcctc agagaagacg agttccctga | 240 | | |
| 156 | gccccggcctt aaacacctcc aacggggatg gctctgaaac agaaaccacc tctgccatcc | 300 | | |

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| | | | | | | | |
|-----|------------|-------------|-------------|-------------|------------|-------------|------|
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| 158 | aacggcagat | cgtagccagc | cagctggagc | gatgcaagct | cggatccgag | actggcagca | 420 |
| 159 | tgagcagcat | gagttcagca | gaagagcagt | ttcagtggca | gtcacaagat | ggtcaaaaag | 480 |
| 160 | atatcgaaga | tgagcttaca | acaggtctcg | agctgggtga | ctcctgtatt | aggctactac | 540 |
| 161 | aggaatcagg | aatacttgac | ccacaggatt | attctacagg | tgaaaggccc | agcctgctct | 600 |
| 162 | cccagagtgc | acttcagctc | aattccaaac | ctgaagggtc | tttccagtat | ccggccagct | 660 |
| 163 | accatagcaa | ccagaccctg | gccctggggg | aaaccacccc | ttcacagctc | ccggcccagag | 720 |
| 164 | gcacacaagc | ccgagctacg | ggccagagct | tcagccaggg | cacgaccagc | cgcgcgggcc | 780 |
| 165 | acctggcggg | gccgagcccc | gcgcgcggcc | cgcgcgggcc | gccgcgggag | ccgttcgcgc | 840 |
| 166 | ccagcctggg | cagcgccttc | caactgcccc | acgcgcggcc | cgcgcgggcc | gccgcgcgcg | 900 |
| 167 | tctactactc | cagctccacg | ctgcccgcgc | cgcgcgcgcg | gggtctcccc | ctggccgcgc | 960 |
| 168 | cccaggcgcg | ttgcgccacc | aaagtgcagc | gcgcgcggctc | ggcccccgag | ggcgccacct | 1020 |
| 169 | acgcgcgcgc | gcgcgcctcc | tcgcgccagc | agtcgcgccg | ccgcctggcc | aagtcctaca | 1080 |
| 170 | gcaccagctc | gccccatcac | atcgctgtgt | cctcgccggg | cctgtccccg | atcccgctga | 1140 |
| 171 | cctcgccccc | caccgtgcag | tcacccatct | cctcctcgcc | catccaccag | ctgagctcca | 1200 |
| 172 | ccatcggcac | gtacgcacc | ctgtgcacca | ccaagcgcc | ggtccacgcg | tcgagcagct | 1260 |
| 173 | acagcaagca | ctcgcaggag | ctgtatgcc | cggccaccct | ccagaggccc | ggcagcctgg | 1320 |
| 174 | cagctgggtc | ccgagcctca | tacagcagcc | agcatggggc | cctgggcccc | gagttgcggg | 1380 |
| 175 | ccctgcagtc | cccagaacac | cacatagatc | ccatctatga | agaccgcgtc | tatcagaagc | 1440 |
| 176 | cccctatgag | gagttctcagc | cagagccagg | gggacctctc | gccgcagca | cacaccggca | 1500 |
| 177 | cctaccgcac | gagcacagcc | ccatcttccc | ctggtgtcga | ctccgtcccc | ttgcagcgca | 1560 |
| 178 | caggcagcca | gcacggcccc | cagaatgcgc | ccgcggccac | cttccagagg | gccagctatg | 1620 |
| 179 | ccgcggggcc | agcctccaat | tacgcggacc | cctaccgaca | gctgcagtat | tgtccctctg | 1680 |
| 180 | ttgagctctc | atacagcaaa | tcgcggccctg | ctctcccgc | tgaaggcacc | ttggccagggt | 1740 |
| 181 | ccccgtccat | tgatagcatt | cagaagatc | ccagagaatt | tgatgggaga | gacccggaac | 1800 |
| 182 | tgccggaagt | gattcagatg | ttgcagcacc | agtttccctc | ggtccagctc | aacgcggcag | 1860 |
| 183 | cctacttgca | acacctctgt | tttggagaca | acaaaattaa | agccgagata | aggagacaa | 1920 |
| 184 | gaggcatcca | gctcctgggtg | gacctgttgg | atcatcgga | gacccaagtc | caccgtagtg | 1980 |
| 185 | cctgtggagc | tctgagaaac | ctggtgtatg | ggaaggccaa | cgatgataac | aaaattgcc | 2040 |
| 186 | tgaaaaactg | tggtggcacc | ccagcactgg | tgaggttact | ccgcaagacg | actgacctgg | 2100 |
| 187 | agatccggga | gctggtcaca | ggagtccttt | ggaacctctc | ctcatgcgat | gcaactcaaa | 2160 |
| 188 | tgccaatcat | ccaggtatgc | ctagcagtac | tgaccaacgc | ggtgattatc | ccccactcag | 2220 |
| 189 | gctgggaaaa | ttcgccctct | caggatgac | ggaaaataca | gctgcattca | tcacagggtg | 2280 |
| 190 | tgcgtaacgc | caccgggtgc | ctaagggaatg | ttagttcggc | cggagaggag | gccgcagaa | 2340 |
| 191 | ggatgagaga | gtgtgatggg | cttacggatg | ccttgctgta | cgtgatccag | tctgcgctgg | 2400 |
| 192 | ggagcagtga | gatcgatagc | aagaccgttg | aaaactgtgt | gtgcatttta | aggaacctct | 2460 |
| 193 | cgtaccggct | ggcggcagaa | acgtctcagg | gacagcacat | gggcacggac | gagctggacg | 2520 |
| 194 | ggctactctg | tgccgaggcc | aatggcaagg | atgctgagag | ctctgggtgc | tggggcaaga | 2580 |
| 195 | agaagaagaa | aaagaaatcc | caagatcagt | gggatggagt | aggacctctt | ccagactgtg | 2640 |
| 196 | ctgaaccacc | aaaagggtac | cagatgctgt | ggcacccatc | aatagtcaaa | ccctacctca | 2700 |
| 197 | cactgtctct | tgagtgtctc | aatccagaca | cgttggaagg | ggcggcaggc | gccctgcaga | 2760 |
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| 203 | ccaagaacat | ggagaacgcc | aaggccttac | gggatgccgg | tggtcagcag | aaattgggtcg | 3120 |
| 204 | gcactctcaa | aaagcaaggga | gataaacact | ctccaaaagt | ggtcaaggct | gcactctcagg | 3180 |
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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/501,171A
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207 cctcctcccg caagccctcc atctcccctg tgcgcgtgtc tcccaacaac cgctcagcaa 3360
208 gtgccccagc ttccacctcg gaaatgatca gctcaaaaga aaggaaaaca gactacgagt 3420
209 gcaccggcag caacgcccacc taccacggag ctaaaggcga acacacttcc aggaaagatg 3480
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226 gtatggattt ccagtttttc tttactttct cccagtatgt tttaacaaaa aaaaaaaaaa 4500
227 gcaggaaaaa aggaatattt agcagtattg ttcgttctga tatgtgaatt tgtttgtgac 4560
228 aactaaacaa ggcattcagc agttttctgac aattaacata catcattcca cactccttgt 4620
229 caacaaagtg ctttttcaact gcctaaaatt ttagatgtag atatttgaaa tagatttttt 4680
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231 ctgtca
232 <210> SEQ ID NO: 4
233 <211> LENGTH: 1225
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242 35 40 45
243 Ser Ala Ile Leu Ala Ser Val Lys Glu Gln Glu Leu Gln Phe Glu Arg
244 50 55 60
245 Leu Thr Arg Glu Leu Glu Ala Glu Arg Gln Ile Val Ala Ser Gln Leu
246 65 70 75 80
247 Glu Arg Cys Lys Leu Gly Ser Glu Thr Gly Ser Met Ser Ser Met Ser
248 85 90 95
249 Ser Ala Glu Glu Gln Phe Gln Trp Gln Ser Gln Asp Gly Gln Lys Asp
250 100 105 110
251 Ile Glu Asp Glu Leu Thr Thr Gly Leu Glu Leu Val Asp Ser Cys Ile
252 115 120 125
253 Arg Ser Leu Gln Glu Ser Gly Ile Leu Asp Pro Gln Asp Tyr Ser Thr
254 130 135 140
255
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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/501,171A

DATE: 06/08/2000

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Input Set : A:\Pto.amc

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date